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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/060,765

DATE: 05/01/2002  
TIME: 11:52:29

Input Set : N:\Crf3\RULE60\10060765.raw  
Output Set: N:\CRF3\05012002\J060765.raw

1 <110> APPLICANT: Itoh, Nobuyuki  
2 Kavanaugh, W. Michael  
3 <120> TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION  
4 PRODUCTS  
5 <130> FILE REFERENCE: PP-16758.001/201130.408  
6 <140> CURRENT APPLICATION NUMBER: 10/060,765  
7 <141> CURRENT FILING DATE: 2002-01-29  
9 <150> PRIOR APPLICATION NUMBER: US/09/715,805  
10 <151> PRIOR FILING DATE: 2000-11-16  
13 <160> NUMBER OF SEQ ID NOS: 17  
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 659  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Mus musculus  
20 <220> FEATURE:  
21 <221> NAME/KEY: CDS  
22 <222> LOCATION: (14)...(646)  
23 <400> SEQUENCE: 1  
24 gagcgcagcc ctg atg gaa tgg atg aga tct aga gtt ggg acc ctg gga 49  
25 Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly  
26 1 5 10  
27 ctg tgg gtc cga ctg ctg gct gtc ttc ctg ctg ggg gtc tac caa 97  
28 Leu Trp Val Arg Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln  
29 15 20 25  
30 gca tac ccc atc cct gac tcc agc ccc ctc ctc cag ttt ggg ggt caa 145  
31 Ala Tyr Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln  
32 30 35 40  
33 gtc cgg cag agg tac ctc tac aca gat gac gac caa gac act gaa gcc 193  
34 Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala  
35 45 50 55 60  
36 cac ctg gag atc agg gag gat gga aca gtg gta ggc gca gca cac cgc 241  
37 His Leu Glu Ile Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg  
38 65 70 75  
39 agt cca gaa agt ctc ctg gag ctc aaa gcc ttg aag cca ggg gtc att 289  
40 Ser Pro Glu Ser Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile  
41 80 85 90  
42 caa atc ctg ggt gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat 337  
43 Gln Ile Leu Gly Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp  
44 95 100 105  
45 gga gct ctc tat gga tcg cct cac ttt gat cct gag gcc tgc agc ttc 385  
46 Gly Ala Leu Tyr Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe  
47 110 115 120

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48	aga gaa ctg ctg ctg gag gac ggt tac aat gtg tac cag tct gaa gcc	433
49	Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala	
50	125 130 135 140	
51	cat ggc ctg ccc ctg cgt ctg cct cag aag gac tcc cca aac cag gat	481
52	His Gly Leu Pro Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp	
53	145 150 155	
54	gca aca tcc tgg gga cct gtg cgc ttc ctg ccc atg cca ggc ctg ctc	529
55	Ala Thr Ser Trp Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu	
56	160 165 170	
57	cac gag ccc caa gac caa gca gga ttc ctg ccc cca gag ccc cca gat	577
58	His Glu Pro Gln Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp	
59	175 180 185	
60	gtg ggc tcc tct gac ccc ctg agc atg gta gag cct tta cag ggc cga	625
61	Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg	
62	190 195 200	
63	agc ccc agc tat gcg tcc tga ctcttcctga atc	659
64	Ser Pro Ser Tyr Ala Ser *	
65	205 210	
67	<210> SEQ ID NO: 2	
68	<211> LENGTH: 210	
69	<212> TYPE: PRT	
70	<213> ORGANISM: Mus musculus	
71	<400> SEQUENCE: 2	
72	Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly Leu Trp Val Arg	
73	1 5 10 15	
74	Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile	
75	20 25 30	
76	Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg	
77	35 40 45	
78	Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile	
79	50 55 60	
80	Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser	
81	65 70 75 80	
82	Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly	
83	85 90 95	
84	Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr	
85	100 105 110	
86	Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu	
87	115 120 125	
88	Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro	
89	130 135 140	
90	Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp	
91	145 150 155 160	
92	Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln	
93	165 170 175	
94	Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser	
95	180 185 190	
96	Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser Pro Ser Tyr	
97	195 200 205	

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Input Set : N:\Crf3\RULE60\10060765.raw  
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98        Ala Ser  
 99                210  
 101 <210> SEQ ID NO: 3  
 102 <211> LENGTH: 643  
 103 <212> TYPE: DNA  
 104 <213> ORGANISM: Homo sapiens  
 105 <220> FEATURE:  
 106 <221> NAME/KEY: CDS  
 107 <222> LOCATION: (9)...(638)  
 108 <400> SEQUENCE: 3  
 109        agccattg atg gac tcg gac gag acc ggg ttc gag cac tca gga ctg tgg 50  
 110                Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp  
 111                1                5                10  
 112        gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc 98  
 113        Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro  
 114                15                20                25                30  
 115        atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag 146  
 116        Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln  
 117                35                40                45  
 118        cggtt tac ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag 194  
 119        Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu  
 120                50                55                60  
 121        atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa 242  
 122        Ile Arg Glu Asp Gly Thr Val Gly Ala Ala Asp Gln Ser Pro Glu  
 123                65                70                75  
 124        agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg 290  
 125        Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu  
 126                80                85                90  
 127        gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg 338  
 128        Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu  
 129                95                100                105                110  
 130        tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg 386  
 131        Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu  
 132                115                120                125  
 133        ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc 434  
 134        Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu  
 135                130                135                140  
 136        ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc 482  
 137        Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro  
 138                145                150                155  
 139        cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc gca ctc 530  
 140        Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu  
 141                160                165                170  
 142        ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc 578  
 143        Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser  
 144                175                180                185                190  
 145        tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc 626  
 146        Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser  
 147                195                200                205

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Input Set : N:\Crf3\RULE60\10060765.raw  
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148 tac gct tcc tga agcca 643  
 149 Tyr Ala Ser \*  
 151 <210> SEQ ID NO: 4  
 152 <211> LENGTH: 209  
 153 <212> TYPE: PRT  
 154 <213> ORGANISM: Homo sapiens  
 155 <400> SEQUENCE: 4  
 156 Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser  
 157 1 5 10 15  
 158 Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro  
 159 20 25 30  
 160 Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr  
 161 35 40 45  
 162 Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg  
 163 50 55 60  
 164 Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu  
 165 65 70 75 80  
 166 Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val  
 167 85 90 95  
 168 Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly  
 169 100 105 110  
 170 Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu  
 171 115 120 125  
 172 Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu  
 173 130 135 140  
 174 His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly  
 175 145 150 155 160  
 176 Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu  
 177 165 170 175  
 178 Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp  
 179 180 185 190  
 180 Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala  
 181 195 200 205  
 182 Ser  
 184 <210> SEQ ID NO: 5 20  
 185 <211> LENGTH: 20  
 186 <212> TYPE: DNA  
 187 <213> ORGANISM: Artificial Sequence  
 188 <220> FEATURE:  
 189 <223> OTHER INFORMATION: PCR primer  
 190 <400> SEQUENCE: 5  
 191 agccattgtat ggactcggac  
 193 <210> SEQ ID NO: 6  
 194 <211> LENGTH: 20  
 195 <212> TYPE: DNA  
 196 <213> ORGANISM: Artificial Sequence  
 197 <220> FEATURE:  
 198 <223> OTHER INFORMATION: PCR primer  
 199 <400> SEQUENCE: 6

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Input Set : N:\Crf3\RULE60\10060765.raw  
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200 tggcttcagg aagcgttagct 20  
 202 <210> SEQ ID NO: 7  
 203 <211> LENGTH: 16  
 204 <212> TYPE: PRT  
 205 <213> ORGANISM: Homo sapiens  
 206 <400> SEQUENCE: 7  
 207 Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His  
 208 1 5 10 15  
 210 <210> SEQ ID NO: 8  
 211 <211> LENGTH: 15  
 212 <212> TYPE: PRT  
 213 <213> ORGANISM: Homo sapiens  
 214 <400> SEQUENCE: 8  
 215 His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg  
 216 1 5 10 15  
 218 <210> SEQ ID NO: 9  
 219 <211> LENGTH: 218  
 220 <212> TYPE: PRT  
 221 <213> ORGANISM: Mus musculus  
 222 <400> SEQUENCE: 9  
 223 Met Ala Arg Lys Trp Asn Gly Arg Ala Val Ala Arg Ala Leu Val Leu  
 224 1 5 10 15  
 225 Ala Thr Leu Trp Leu Ala Val Ser Gly Arg Pro Leu Ala Gln Gln Ser  
 226 20 25 30  
 227 Gln Ser Val Ser Asp Glu Asp Pro Leu Phe Leu Tyr Gly Trp Gly Lys  
 228 35 40 45  
 229 Ile Thr Arg Leu Gln Tyr Leu Tyr Ser Ala Gly Pro Tyr Val Ser Asn  
 230 50 55 60  
 231 Cys Phe Leu Arg Ile Arg Ser Asp Gly Ser Val Asp Cys Glu Glu Asp  
 232 65 70 75 80  
 233 Gln Asn Glu Arg Asn Leu Leu Glu Phe Arg Ala Val Ala Leu Lys Thr  
 234 85 90 95  
 235 Ile Ala Ile Lys Asp Val Ser Ser Val Arg Tyr Leu Cys Met Ser Ala  
 236 100 105 110  
 237 Asp Gly Lys Ile Tyr Gly Leu Ile Arg Tyr Ser Glu Glu Asp Cys Thr  
 238 115 120 125  
 239 Phe Arg Glu Glu Met Asp Cys Leu Gly Tyr Asn Gln Tyr Arg Ser Met  
 240 130 135 140  
 241 Lys His His Leu His Ile Ile Phe Ile Gln Ala Lys Pro Arg Glu Gln  
 242 145 150 155 160  
 243 Leu Gln Asp Gln Lys Pro Ser Asn Phe Ile Pro Val Phe His Arg Ser  
 244 165 170 175  
 245 Phe Phe Glu Thr Gly Asp Gln Leu Arg Ser Lys Met Phe Ser Leu Pro  
 246 180 185 190  
 247 Leu Glu Ser Asp Ser Met Asp Pro Phe Arg Met Val Glu Asp Val Asp  
 248 195 200 205  
 249 His Leu Val Lys Ser Pro Ser Phe Gln Lys  
 250 210 215  
 252 <210> SEQ ID NO: 10

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10060765.raw  
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